



## SEQUENCE LISTING

<110> Callen, Walter  
Richardson, Toby  
Frey, Gerhard  
Miller, Carl  
Kazaoka, Martin  
Short, Jay  
Mathur, Eric

<120> ENZYMES HAVING ALPHA AMYLASE ACTIVITY  
AND METHODS OF USE THEREOF

<130> 09010-107001

<140> 10/081,739

<141> 2002-02-21

<150> 60/270,495

<151> 2001-02-21

<150> 60/270,496

<151> 2001-02-21

<150> 60/291,122

<151> 2001-05-14

<160> 69

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1311

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated

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<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically engineered

<400> 2

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
35          40          45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50          55          60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65          70          75          80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85          90          95
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100         105         110
Arg Ala Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
115         120         125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
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Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
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Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165         170         175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180         185         190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
195         200         205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
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225         230         235         240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
245         250         255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
260         265         270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
275         280         285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
290         295         300
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305         310         315         320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Glu Asn

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385			390		395					400					
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	405		410		415										
Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr
	420		425		430										
Cys	Gly	Val	Gly												
	435														

&lt;210&gt; 3

&lt;211&gt; 1419

&lt;212&gt; DNA

&lt;213&gt; Environmental

&lt;400&gt; 3

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&lt;211&gt; 1539

&lt;212&gt; DNA

&lt;213&gt; Environmental

&lt;400&gt; 4

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&lt;210&gt; 5

&lt;211&gt; 1395

&lt;212&gt; DNA

&lt;213&gt; Environmental

&lt;400&gt; 5

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&lt;210&gt; 6

&lt;211&gt; 1386

&lt;212&gt; DNA

## &lt;213&gt; Bacteria

&lt;400&gt; 6

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&lt;210&gt; 7

&lt;211&gt; 472

&lt;212&gt; PRT

&lt;213&gt; Environmental

&lt;400&gt; 7

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Tyr	Phe	Glu	Trp	Tyr	Leu	Pro	Asp	Asp	Gly	Thr	Leu	Trp	Thr	Lys	Val
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Leu	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly
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Val	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val
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Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His	Asp																			
															465					470					475									
Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly	Trp																			
															485					490					495									
Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln	Arg																			
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&lt;210&gt; 9

&lt;211&gt; 464

&lt;212&gt; PRT

&lt;213&gt; Environmental

&lt;400&gt; 9

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Ala	Ser	Ile	Gly	Leu	Leu	Ser	Thr	Pro	Val	Gly	Ala	Ala	Lys	Tyr	Ser
			20					25					30		
Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Met	Gln	Ala	Phe	Tyr	Trp	Asp	Val
		35					40					45			
Pro	Gly	Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Arg	Gln	Lys	Ile	Pro	Glu
	50					55					60				
Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser	Lys
65					70					75					80
Gly	Met	Gly	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Phe	Phe
				85					90					95	
Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe	Gly
			100					105					110		
Ser	Lys	Glu	Glu	Leu	Val	Asn	Met	Ile	Asn	Thr	Ala	His	Ser	Tyr	Gly
			115				120					125			
Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly	Asp
	130					135					140				
Leu	Glu	Trp	Asn	Pro	Phe	Val	Asn	Asn	Tyr	Thr	Trp	Thr	Asp	Phe	Ser
145					150					155					160
Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His	Pro
				165					170					175	
Asn	Glu	Val	Lys	Cys	Cys	Asp	Glu	Gly	Thr	Phe	Gly	Asp	Phe	Pro	Asp
			180					185					190		
Ile	Ala	His	Glu	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	Trp	Ala	Ser	Asn
	195					200						205			
Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile	Asp	Ala	Trp	Arg
	210					215					220				
Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val	Val	Asn	Asp	Trp	Leu
225					230					235					240
Ser	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn	Val
			245						250					255	
Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Asp	Ser	Gly	Ala	Lys	Val	Phe	Asp
			260					265					270		
Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Glu	Ala	Phe	Asp	Asn	Thr	Asn	Ile
	275						280					285			
Pro	Ala	Leu	Val	Tyr	Ala	Leu	Gln	Asn	Gly	Gly	Thr	Val	Val	Ser	Arg
	290					295					300				
Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	His	Asp	Thr	Asp	Ile
305					310					315					320
Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Tyr	Glu	Gly
			325						330					335	
Gln	Pro	Val	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu	Trp	Leu	Asn	Lys	Asp
			340					345					350		
Lys	Leu	Asn	Asn	Leu	Ile	Trp	Ile	His	Glu	His	Leu	Ala	Gly	Gly	Ser
	355						360					365			
Thr	Lys	Ile	Leu	Tyr	Tyr	Asp	Asn	Asp	Glu	Leu	Ile	Phe	Met	Arg	Glu
	370					375					380				
Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	Ile	Asn	Leu	Gly	Asn
385					390					395					400
Asp	Trp	Ala	Glu	Arg	Trp	Val	Asn	Val	Gly	Ser	Lys	Phe	Ala	Gly	Tyr
			405						410					415	
Thr	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	Val	Asp	Arg	Trp
			420					425					430		
Val	Gln	Tyr	Asp	Gly	Trp	Val	Lys	Leu	Thr	Ala	Pro	Pro	His	Asp	Pro
		435					440					445			



Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Ala Gly Val Gly  
 450 455 460

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 1 5 10 15  
 Met Ala Val Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu  
 20 25 30  
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 35 40 45  
 Gly Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr  
 50 55 60  
 Glu Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met  
 65 70 75 80  
 Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu  
 85 90 95  
 Gly Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys  
 100 105 110  
 Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys  
 115 120 125  
 Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu  
 130 135 140  
 Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val  
 145 150 155 160  
 Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu  
 165 170 175  
 Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala  
 180 185 190  
 His Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser  
 195 200 205  
 Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp  
 210 215 220  
 Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp  
 225 230 235 240  
 Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala  
 245 250 255  
 Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro  
 260 265 270  
 Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala  
 275 280 285  
 Leu Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro  
 290 295 300  
 Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp  
 305 310 315 320  
 Asn Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro  
 325 330 335  
 Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu  
 340 345 350  
 Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser  
 355 360 365  
 Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr  
 370 375 380

Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys  
 385 390 395 400  
 Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His  
 405 410 415  
 Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser  
 420 425 430  
 Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly  
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39

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<400> 13  
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33

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38

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33

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32

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38

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<400> 18  
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35

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<400> 20

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36

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<212> DNA

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<223> Primer

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31

<210> 24

<211> 30

<212> DNA

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<220>

<223> Primer

<400> 24

gaacgtctca ttgtagtaga gcgggaagtc

30

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<400> 26

gaaccgtctc acttcacact gcgaggtggt c

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31

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<211> 33

<212> DNA

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<400> 28

tcgagactga ctctcaccca acaccgcaat agc

33

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50

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<400> 46

tcgagactga ctctcagccc accccgcagt agctc

35

<210> 47

<211> 50

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<210> 48

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30

<210> 49

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<400> 49

gaaccgtctc aaaacaccgc ccacgcctat g

31

<210> 50

<211> 33

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<400> 50

gaacgtctca cctcgacttc caccgaacg agc

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31

<210> 52

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<212> DNA

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<400> 52

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32

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<211> 30

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gaaccgtctc acgatataat ctggaacaag

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<211> 35

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gaaccgtctc agaagcactg acatcgttta ctacg

35

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 gcgatatgga tccctcccgc gagcaagggg atgagcggcg gctattcgat gggctacgac 180  
 ccctacgatt attttgacct cggtagtgc taccagaagg gaacggtgga aacgaggttc 240  
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atagccgata	tagtcatcaa	ccaccgcgcc	ggcggtgacc	tggagtggaa	ccccttcgtg	360
aacgactata	cctggaccga	cttctcaaag	gtcgcgtcgg	gtaaatacac	ggccaactac	420
ctcgacttcc	acccgaacga	gtcccatgcg	ggcgattccg	gaacatttgg	aggctatccc	480
gacatatgcc	acgacaagag	ctgggaccag	tactggctct	gggccagcca	ggagagctac	540
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ttttagtcca	accacgatac	cgacataatc	tggaaacaagt	atccagccta	cgcgttcatc	900
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gataagctca	agaacctcat	ctggatacat	gacaacctcg	ccggagggag	cactgacatc	1020
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ttcgcaggct	cgtgcataca	cgagtacacc	ggcaatctcg	gcggctgggt	ggacaagtgg	1200
gtggactcaa	gcggctgggt	ctacctcgag	gctcctgccc	acgaccgggc	caacggccag	1260
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&lt;210&gt; 67

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Environmental

&lt;400&gt; 67

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1				5					10					15	
Val	Pro	Met	Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Ala	Gln	Lys	Ile	Pro
			20					25					30		
Asp	Trp	Ala	Ser	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser
		35					40					45			
Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Tyr
	50					55					60				
Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe
65					70					75					80
Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr	Ala	His	Ala	Tyr
				85					90					95	
Gly	Met	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly
			100					105					110		
Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Asn	Asp	Tyr	Thr	Trp	Thr	Asp	Phe
			115				120					125			
Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His
	130					135					140				
Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe	Gly	Gly	Tyr	Pro
145				150						155					160
Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	Trp	Ala	Ser
			165						170					175	
Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile	Asp	Ala	Trp
			180					185					190		
Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Ala	Pro	Trp	Val	Val	Lys	Asp	Trp
		195					200					205			
Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn
	210					215					220				
Val	Asp	Ala	Val	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	Ala	Lys	Val	Phe
225				230						235					240
Asp	Phe	Ala	Leu	Tyr	Tyr	Lys	Met	Asp	Glu	Ala	Phe	Asp	Asn	Asn	Asn
			245						250				255		
Ile	Pro	Ala	Leu	Val	Asp	Ala	Leu	Arg	Tyr	Gly	Gln	Thr	Val	Val	Ser

260	265	270
Arg Asp Pro Phe Lys Ala Val Thr	Phe Val Ala Asn His Asp Thr Asp	
275	280	285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe	Ile Leu Thr Tyr Glu	
290	295	300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu	Glu Trp Leu Asn Lys	
305	310	315
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp	Asn Leu Ala Gly Gly	
325	330	335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu	Leu Ile Phe Val Arg	
340	345	350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr	Ile Asn Leu Ala	
355	360	365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro	Lys Phe Ala Gly Ser	
370	375	380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly	Trp Val Asp Lys Trp	
385	390	395
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala	Pro Ala His Asp Pro	
405	410	415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr	Cys Gly Val Gly	
420	425	430

<210> 68  
 <211> 1386  
 <212> DNA  
 <213> Bacteria

<400> 68	
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gcccagcccc cgggggcggc caagtacctg gagctcgaag agggcggcgt cataatgcag	120
gcgttctact gggacgtgcc ttcaggagga atatggtggg acacaatacg gcagaagata	180
ccggagtggt acgatgccgg aatctccgca atatggattc ccccggcgag caagggcag	240
ggcggcgcct attcgatggg ctacgacccc tacgacttct ttgacctcgg tgagtacgac	300
cagaagggaa cggtagagac gcgctttggc tccaagcagg agctcgtgaa catgataaac	360
accgcccacg cctacggcat caaggtcatc gcagacatag taatcaacca ccgcgccgga	420
ggagaccttg agtggaaccc cttcgtcaat gactacacct ggacggactt ctcgaagggtc	480
gcttccggca agtacacggc caactacctc gacttccacc ccaacgaggt caagtgctgc	540
gacgagggca cctttggagg gttcccgga atagcccacg agaagagctg ggaccagtac	600
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tggcgcttcg actacgtcaa gggctacgga gcgtgggtcg tcaaggactg gctggactgg	720
tggggagggt gggccgtcgg ggagtactgg gacacaaacg ttgatgcact gctcaactgg	780
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agccgcgacc cgtttaaggc cgtaaccttc gttgcaaacc acgacacgga cataatttgg	960
aacaagtacc cggcctacgc cttcatctc acctacgagg gccagccgac gatattctac	1020
cgcgactacg aggagtggct caacaaggac aggtcaaga acctcatctg gatacacgac	1080
caactcgccg gtggaagcac cgacatagtc tactacgata acgatgaact catcttcgtc	1140
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gccgggaggt ggggtctacgt tccgaagttc gccgggagcgt gcatccacga gtacaccggc	1260
aacctcggcg gctgggtgga caagtgggtg gactcaagcg ggtgggtgta cctcgaggcc	1320
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ggctga	1386

<210> 69  
 <211> 461  
 <212> PRT  
 <213> Bacteria

&lt;400&gt; 69

Met	Lys	Pro	Ala	Lys	Leu	Leu	Val	Phe	Val	Leu	Val	Val	Ser	Ile	Leu
1				5					10					15	
Ala	Gly	Leu	Tyr	Ala	Gln	Pro	Ala	Gly	Ala	Ala	Lys	Tyr	Leu	Glu	Leu
			20					25					30		
Glu	Glu	Gly	Gly	Val	Ile	Met	Gln	Ala	Phe	Tyr	Trp	Asp	Val	Pro	Ser
		35					40					45			
Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Arg	Gln	Lys	Ile	Pro	Glu	Trp	Tyr
	50					55					60				
Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser	Lys	Gly	Met
65					70					75					80
Gly	Gly	Ala	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Phe	Phe	Asp	Leu
				85					90					95	
Gly	Glu	Tyr	Asp	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe	Gly	Ser	Lys
			100					105					110		
Gln	Glu	Leu	Val	Asn	Met	Ile	Asn	Thr	Ala	His	Ala	Tyr	Gly	Ile	Lys
		115					120					125			
Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly	Asp	Leu	Glu
	130					135					140				
Trp	Asn	Pro	Phe	Val	Asn	Asp	Tyr	Thr	Trp	Thr	Asp	Phe	Ser	Lys	Val
145					150					155					160
Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His	Pro	Asn	Glu
				165					170					175	
Val	Lys	Cys	Cys	Asp	Glu	Gly	Thr	Phe	Gly	Gly	Phe	Pro	Asp	Ile	Ala
			180					185					190		
His	Glu	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	Trp	Ala	Ser	Asn	Glu	Ser
	195					200						205			
Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Val	Asp	Ala	Trp	Arg	Phe	Asp
	210					215					220				
Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val	Val	Lys	Asp	Trp	Leu	Asp	Trp
225					230					235					240
Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn	Val	Asp	Ala
			245						250					255	
Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Asp	Ala	Lys	Val	Phe	Asp	Phe	Pro
			260					265					270		
Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe	Asp	Asn	Lys	Asn	Ile	Pro	Ala
			275				280					285			
Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly	Thr	Val	Val	Ser	Arg	Asp	Pro
	290					295					300				
Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	His	Asp	Thr	Asp	Ile	Ile	Trp
305					310					315					320
Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Tyr	Glu	Gly	Gln	Pro
			325						330					335	
Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu	Trp	Leu	Asn	Lys	Asp	Arg	Leu
			340					345					350		
Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	His	Leu	Ala	Gly	Gly	Ser	Thr	Asp
		355					360					365			
Ile	Val	Tyr	Tyr	Asp	Asn	Asp	Glu	Leu	Ile	Phe	Val	Arg	Asn	Gly	Tyr
	370					375					380				
Gly	Asp	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	Ile	Asn	Leu	Gly	Ser	Ser	Lys
385					390					395					400
Ala	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys	Phe	Ala	Gly	Ala	Cys	Ile	His
			405						410					415	
Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	Val	Asp	Lys	Trp	Val	Asp	Ser
			420				425					430			
Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro	Ala	His	Asp	Pro	Ala	Asn	Gly

		435					440					445
Tyr	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr	Cys	Gly	Val	Gly
450						455						460